

RESULT 1  
IL2B\_PIG  
ID IL2B\_PIG STANDARD; PRT; 324 AA.  
AC Q28938;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte  
DE maturation factor 40 kDa subunit) (CLMF p40).  
GN IL2B.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=97383978; PubMed=9239844;  
RA Foss D.L., Murtaugh M.P.;  
RT "Molecular cloning and mRNA expression of porcine interleukin-12.";  
RL Vet. Immunol. Immunopathol. 57:121-134(1997).  
CC -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T  
CC AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-  
CC ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA  
CC BY RESTING PBMC (BY SIMILARITY).  
CC -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa  
CC SUBUNITS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
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DR EMBL; U08317; AAA75356.1; -.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003530; Hemtopoptn\_L\_F3.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003598; Ig\_c2.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS01354; HEMATOPO\_REC\_L\_F3; 1.  
KW Cytokine; Glycoprotein; Immunoglobulin domain; Signal.  
FT SIGNAL 1 22 BY SIMILARITY.  
FT CHAIN 23 324 INTERLEUKIN-12 BETA CHAIN.  
FT DOMAIN 43 97 IG-LIKE C2-TYPE DOMAIN.  
FT DOMAIN 231 316 FIBRONECTIN TYPE-III.  
FT DISULFID 50 90 POTENTIAL.  
FT DISULFID 195 195 INTERCHAIN (PROBABLE).  
FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).  
  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 324 AA; 36828 MW; F0E48B72F700086C CRC64;  
  
Query Match 90.7%; Score 1578; DB 1; Length 324;  
Best Local Similarity 90.7%; Pred. No. 1.8e-127;  
Matches 291; Conservative 15; Mismatches 15; Indels 0; Gaps 0;  
  
QY 4 QQLVISWFSVLVLLASPLMAIWELKKDVIYVVELDWYPNAPGETVVLTCDTPEEDGITWTS 63  
Db 4 QQLVVSWSFSLVWLASPIVAIWELEKNVYVVELDWYPNAPGEMVVLTCNTPEEDGITWTS 63  
  
QY 64 QSSEVLGTGKTLTIHVKEFGDAGQYTCRKGGEALSRSLLLBKKEGDIWSTDILKDQEP 123  
Db 64 QSSEVLGTGKTLTIHVKEFGDAGQYTCRKGGAVALSQSLLLBKKEGDIWSTDILKDQEP 123  
  
QY 124 KNKSFLKCEAKNYSGRFTCWLLTISTDLKFSVKSSRGSTDPRGVTCTATLSEDLGEYK 183  
Db 124 KNKSFLKCEAKNYSGRFTCWLLTAISTDLKFSVKSSRGSTDPRGVTCTATLSEDLGEYK 183  
  
QY 184 KYRVECQEGSACPAAEESLPIEVVLEAVHKLKYENYTSFFIRDIKPDPPKNLQKLPLK 243  
Db 184 KYRVECQEGSACPAAEESLPIEVVLEAVHKLKYENYTSFFIRDIKPDPPKNLQKLPLK 243  
  
QY 244 NSRHVEVSWGYPDTWSTPHSYFSLTFQIQVGKSKREKKDRIFTDKTSATVICRKNKAKIR 303  
Db 244 NSRHVEISWEYPTWSTPHSYFSLMFGVQVGKSKREKKDKLFTDQISAKVTCHKKANIR 303  
  
QY 304 VQARDRIYSSFWSEWASVSCS 324  
Db 304 VQARDRIYSSSWSEWASVSCN 324

RESULT 14  
 AR052857  
 LOCUS AR052857 1018 bp DNA linear PAT 29-SEP-1998  
 DEFINITION Sequence 194 from patent US 5833975.  
 ACCESSION AR052857  
 VERSION AR052857.1 GI:5977719  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED.  
 REFERENCE 1 (bases 1 to 1018)  
 AUTHORS Paoletti, E., Tartaglia, J. and Cox, W. I.  
 TITLE Canarypox virus expressing cytokine and/or tumor-associated antigen  
 JOURNAL DNA sequence  
 Patent: US 5833975-A 194 10-NOV-1998;  
 FEATURES Location/Qualifiers  
 source 1..1018  
 /organism="unknown"  
 BASE COUNT 283 a 245 c 260 g 230 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 7.77e-142 Length: 1018  
 Score: 1539.00 Matches: 288  
 Percent Similarity: 92.10% Conservative: 15  
 Best Local Similarity: 87.54% Mismatches: 20  
 Query Match: 88.45% Indels: 6  
 DB: 6 Gaps: 2

US-09-725-324A-8 (1-324) x AR052857 (1-1018)

Qy 1 MetCysHisGlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeu 20  
 Db 32 ATGTGTCAACAGCAGTGTGGTCATCTCTGGTTTCCCTGGTTTCTGGCATCTCCCTC 91  
 Qy 21 MetAlaIleTrpGluLeuLysLysAspValTyrValValGluLeuAspTrpTyrProAsn 40  
 Db 92 GTGGCCATATGGGAAGTGAAGAAAGATGTTATGTCGTAGAAATTGGATGGTATCCGGAT 151  
 Qy 41 AlaProGlyGluThrValValLeuThrCysAspThrProGluGluAspGlyIleThrTrp 60  
 Db 152 GCCCTGGAGAAATGGTGGTCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 211  
 Qy 61 ThrSerAspGlnSerSerGluValLeuGlyThrGlyLysThrLeuThrIleHisValLys 80  
 Db 212 ACCTTGGACCAAGAGCAGTGGGCTTAGGCTCTGGCAAAACCTGACCATCAAGTCAAA 271  
 Qy 81 GluPheGlyAspAlaGlyGlnTyrThrCysArgLysGlyGlyGluAlaLeuSerArgSer 100  
 Db 272 GAGTTTGGAGATGCTGGCCAGTACACCTGTACAAAGGAGGCGAGGTCTAAGCCATTGC 331  
 Qy 101 LeuLeuLeuLeuHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysAspGln 120  
 Db 332 CTCCTGCTGCTTCAAAAAGGAAGATGGAATTTGGTCCACTGATATTTAAAGGACCAG 391  
 Qy 121 LysGluProLysAsnLysSerPheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140  
 Db 392 AAAGAACCACAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATCTGGACGTTTC 451  
 Qy 141 ThrCysTrpTrpLeuThrThrIleSerThrAspLeuLysPheSerValLysSerSerArg 160  
 Db 452 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTGACATTGAGTCAAAAGCAGCAGA 511  
 Qy 161 GlySerThrAspProArgGlyValThrCysGlyThrAlaThrLeuSerGlu----- 177  
 Db 512 GGCTCTTCTGACCCCAAGGGGTGACGTGCGGAGCTGTACACTCTCTGCAGAGAGAGTC 571  
 Qy 178 -----AspLeuGlyGluTyrLysLysTyrArgValGluCysGlnGluGlySerAlaCys 195  
 Db 572 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGACAGTGCCTGC 628  
 Qy 196 ProAlaAlaGluGluSerLeuProIleGluValValLeuGluAlaValHisLysLeuLys 215  
 Db 629 CCAGCTGCTGAGGAGAGTCTGCCATTGAGGTTCATGGTGGATGCCGTTTCAAGCTCAAG 688  
 Qy 216 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 235  
 Db 689 TATGAAACTACACAGCAGCTTCTTCATCAGGGACATCATCAACCTGACCCACCCAAAG 748  
 Qy 236 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGlyTyrPro-255  
 Db 749 AACTTGACAGTGAAGCCATTAAAGAATTCTCGGAGGTGGAGGTGAGTGGGAGTACCT 808  
 Qy 256 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnValGlnGly 275  
 Db 809 GACACCTGGAGTACTCCACATTCTACTTCTCCCTGACATTCTGCGTTGAGGTCCAGGGC 868  
 Qy 276 LysSerLysArgGluLysLysAspArgIlePheThrAspLysThrSerAlaThrValIle 295  
 Db 869 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTACGGACAAGACCTCAGCCACGGTCATC 928  
 Qy 296 CysArgLysAsnAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerPheTrp 315  
 Db 929 TGCCGCAAAATGCCAGCATTAGCGTGGGGCCAGGACCGCTACTATAGTCTATCTTGG 988  
 Qy 316 SerGluTrpAlaSerValSerCysSer 324  
 Db 989 AGCGAATGGGCATCTGTGCCCTGCAGT 1015